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OM protein - protein search, using sw model

Run on: August 28, 2003, 18:27:17 ; Search time 28.9091 Seconds
(without alignments)
107.116 Million cell updates/sec

Title: us-09-743-225-8
Perfect score: 58
Sequence: 1 NTLKTPRVGGXA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	69.0	268	5 Q9XZX5	Q9XZX5 leishmania
2	38	65.5	334	2 Q9F937	Q9F937 pseudomonas
3	38	65.5	742	3 Q9HG15	Q9HG15 yarrowia 11
4	38	65.5	991	3 Q12252	Q12252 saccharomyc
5	37	63.8	388	16 Q8G3N7	Q8G3N7 bifidobacte
6	36	62.1	257	16 Q9CGF3	Q9CGF3 lactococcus
7	36	62.1	266	10 Q9FZ93	Q9FZ93 arabidopsis
8	36	62.1	266	10 Q8GWE8	Q8GWE8 arabidopsis
9	36	62.1	319	10 Q9LRT3	Q9LRT3 arabidopsis
10	36	62.1	409	16 Q8EIH7	Q8EIH7 shewanella
11	36	62.1	1002	2 Q8GM78	Q8GM78 haemophilus
12	36	62.1	1004	2 Q8GM77	Q8GM77 haemophilus
13	36	62.1	1301	12 Q9EMI5	Q9EMI5 ansacta moo
14	35	60.3	132	4 Q8N8V9	Q8N8V9 homo sapien
15	35	60.3	143	12 Q8BC65	Q8BC65 human papil
16	35	60.3	149	16 Q98M54	Q98M54 rhizobium 1

17	35	60.3	235	16 Q8ZRN2	Q8ZRN2 salmonella
18	35	60.3	235	16 Q8Z993	Q8Z993 salmonella
19	35	60.3	235	16 Q8X8W1	Q8X8W1 escherichia
20	35	60.3	306	16 Q8FM02	Q8FM02 corynebacte
21	35	60.3	310	5 Q20160	Q20160 caenorhabdi
22	35	60.3	324	16 Q8P8P9	Q8P8P9 xanthomonas
23	35	60.3	339	2 Q8KI09	Q8KI09 pseudomonas
24	35	60.3	339	2 Q8KIT9	Q8KIT9 pseudomonas
25	35	60.3	340	16 Q8PEV4	Q8PEV4 xanthomonas
26	35	60.3	341	2 Q8GHQ4	Q8GHQ4 pseudomonas
27	35	60.3	353	16 Q9KDZ1	Q9KDZ1 bacillus ha
28	35	60.3	357	16 Q66804	Q66804 aquifex ase
29	35	60.3	413	16 Q8ZHH9	Q8ZHH9 yersinia pe
30	35	60.3	447	16 Q8CZW0	Q8CZW0 yersinia pe
31	35	60.3	456	10 Q8L8A1	Q8L8A1 arabidopsis
32	35	60.3	456	10 Q8LEU4	Q8LEU4 arabidopsis
33	35	60.3	456	10 Q8GWW8	Q8GWW8 arabidopsis
34	35	60.3	461	10 Q9FI35	Q9FI35 arabidopsis
35	35	60.3	514	5 Q21458	Q21458 caenorhabdi
36	35	60.3	530	10 Q8H979	Q8H979 rhus vernic
37	35	60.3	533	10 Q94ID0	Q94ID0 rhus vernic
38	35	60.3	550	16 Q8XR68	Q8XR68 raistonia s
39	35	60.3	637	17 Q972X6	Q972X6 sulfobolus
40	35	60.3	1592	5 Q01583	Q01583 caenorhabdi
41	35	60.3	2591	2 Q54959	Q54959 streptomyce
42	34	58.6	127	3 Q9HEU8	Q9HEU8 emericella
43	34	58.6	177	4 Q8N7V0	Q8N7V0 homo sapien
44	34	58.6	185	5 Q9NKU2	Q9NKU2 leishmania
45	34	58.6	229	5 Q8MPN9	Q8MPN9 drosophila

ALIGNMENTS

RESULT 1

Q9XZX5 PRELIMINARY; PRT; 268 AA.
AC Q9XZX5
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 30.3 kDa protein.
GN L2743.07.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Ivens A.C., Murphy L., Quail M., Harris D., Oliver K., Lawson D.,
RA Rajandream M.A., Barrell B.G.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL389894; CAC22688.1;
KW Hypothetical protein.
SQ SEQUENCE 268 AA; 30293 MW; D68B62C0ADD5444 CRC64;

Query Match 69.0%; Score 40; DB 5; Length 268;

Best Local Similarity 66.7%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NTLKTPRVGGXA 12

Db 200 NPKTPRTGGAA 211

RESULT 2

Q9F937 PRELIMINARY; PRT: 334 AA.
 ID Q9F937
 AC Q9F937
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Glycosyltransferase L.
 GN WPPL
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KT2440;
 RA Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.L.;
 RT "Characterization of a Pseudomonas putida wbpL mutant."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF209871; AAG12993.1;
 DR InterPro; IPR000715; Glyco.trans.4.
 DR Pfam; PF00953; Glycos_transf_4.1.
 KW Transferase.
 SQ SEQUENCE 334 AA; 35637 MW; 1B9372E230A9F842 CRC64;

Query Match 65.5%; Score 38; DB 2; Length 334;
 Best Local Similarity 66.7%; Pred. No. 34;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTLKTPRVGGXA 12
 DB 38 HTLPTPRGGGLA 49
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RESULT 3

Q9HG15 PRELIMINARY; PRT: 742 AA.
 ID Q9HG15
 AC Q9HG15
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Polypeptide release factor 3.
 GN SUP35.
 OS Yarrowia lipolytica (Candida lipolytica).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxID=4952;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21324710; PubMed=11430816;
 RA Nakavashiki T., Ebihara K., Bannai H., Nakamura Y.;
 RT "Yeast [PSI+] 'prions' that are cross-transmissible and susceptible
 RT beyond a species barrier through a quasi-prion state."
 RL Mol. Cell 7:1121-1130(2001).
 DR EMBL; AB039752; BAB12683.1;
 DR InterPro; IPR004160; EFTU_Cterm.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR000795; EF_GTPbind.
 DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 DR Pfam; PF03143; GTP_EFTU_D3; 1.
 DR PRINTS; PR00315; ELONGATNFCT.
 KW GTP-binding; Protein biosynthesis.
 SQ SEQUENCE 742 AA; 80125 MW; 3C8D3F5738206C0A CRC64;

Query Match 65.5%; Score 38; DB 3; Length 742;
 Best Local Similarity 70.0%; Pred. No. 79;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NTLKTPRVGG 10
 DB 172 NKLKPRVGG 181
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RESULT 4

Q12252 PRELIMINARY; PRT: 991 AA.
 ID Q12252
 AC Q12252
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE ORF YOL084W from chromosome XV.
 GN PHM7 OR YOL084W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FY1679;
 RX MEDLINE=96021609; PubMed=8533473;
 RA Zumbstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
 RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
 RT more than twice as many unknown as known open reading frames."
 RL Yeast 11:975-986(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zumbstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X83121; CAA58195.1;
 DR EMBL; Z74826; CAA99096.1;
 DR SGD; S0003444; PHM7.
 DR InterPro; IPR003864; DUF221.
 DR Pfam; PF02714; DUF221; 1.
 SQ SEQUENCE 991 AA; 112545 MW; 491FAB0BD143DC5E CRC64;

Query Match 65.5%; Score 38; DB 3; Length 991;
 Best Local Similarity 77.8%; Pred. No. 11e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NTLKTPRVG 9
 DB 569 NTLATPRMG 577
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RESULT 5

Q8G3N7 PRELIMINARY; PRT: 388 AA.
 ID Q8G3N7
 AC Q8G3N7
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Possible undecaprenyl-phosphate
 DE alpha-N-acetylglucosaminyltransferase.
 GN RFE OR BL1721
 OS Bifidobacterium longum.
 OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
 OC Bifidobacteriaceae; Bifidobacterium.
 OX NCBI_TaxID=216816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCC 2705;
 RA MEDLINE=22294977; PubMed=12381787;
 RA Scheil M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
 RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
 RA Pridmore R.D., Arigoni F.;
 RT "The genome sequence of Bifidobacterium longum reflects its adaptation
 RT to the human gastrointestinal tract."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
 DR EMBL; AE014806; AAN25503.1;
 KW Complete proteome.
 SQ SEQUENCE 388 AA; 41434 MW; COA14679F63A1DD5 CRC64;

RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
PL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

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RT clones";
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
RA Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
RA Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M.,
RA Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W.,
RA Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RN [5]
RL Genome Biol. 0:0-0(2002).
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
DR EMBL; AF024034; BAB02804.1; -
DR EMBL; AF361582; AAK32750.1; -
DR EMBL; AY087770; AAM5305.1; -
DR EMBL; AX133557; AAM91387.1; -
DR HSSP; P07135; IHMF.
DR InterPro; IPR001606; ARID.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF01388; ARID; 1.
DR Pfam; PF00505; HMG_box; 1.
KW Hypothetical protein.
SQ SEQUENCE 319 AA; 36296 MW; 7802A12A69F7456C CRC64;

Query Match 62.1%; Score 36; DB 10; Length 319;
Best Local Similarity 77.8%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TLKTPRVGG 10
DB 60 TLKVPVGG 68

RESULT 10
Q8EIH7 PRELIMINARY; PRT; 409 AA.
AC Q8EIH7;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE D-3-phosphoglycerate dehydrogenase.
GN SERA OR S00862.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-MR-1;
RX MEDLINE-22297566; PubMed-12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Neeson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015531; AAN53938.1; -
DR TIGR; S00862; -
KW Complete proteome.
SQ SEQUENCE 409 AA; 44314 MW; DCA4DD5D3AD7E2B0 CRC64;

Query Match 62.1%; Score 36; DB 16; Length 409;
Best Local Similarity 70.0%; Pred. No. 11e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NTLKTPRVGG 10
DB 286 NVLLTPHVG 295

RESULT 11
Q8GM78 PRELIMINARY; PRT; 1002 AA.
AC Q8GM78;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Adhesin.
GN HIA.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-nontypable strain 3248A;
RX MEDLINE-22300350; PubMed-12410830;
RA Laarmann S., Cutter D., Juehne T., Barenkamp S.J., St Geme J.W.;
RT "The Haemophilus influenzae Hia autotransporter harbours two adhesive
RT pockets that reside in the passenger domain and recognize the same
RT host cell receptor.";
RL Mol. Microbiol. 46:731-743(2002).
DR EMBL; AY078085; AAL79951.1; -
SQ SEQUENCE 1002 AA; 103638 MW; F9C4130DC2C37EAE CRC64;

Query Match 62.1%; Score 36; DB 2; Length 1002;
Best Local Similarity 70.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NTLKTPRVGG 10
DB 222 STLDPRVGG 231

RESULT 12
Q8GM77 PRELIMINARY; PRT; 1004 AA.
AC Q8GM77;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Adhesin.
GN HIA.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.

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OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=non-typeable strain 1862A;
 RX MEDLINE=22300350; PubMed=12410830;
 RA Laarmann S., Cutter D., Juehne T., Barenkamp S.J., St Geme J.W.;
 RT "The Haemophilus influenzae Hia autotransporter harbours two adhesive
 RT pockets that reside in the passenger domain and recognize the same
 RT host cell receptor";
 RL Mol. Microbiol. 46:731-743(2002).
 DR EMBL: AY078086; AAL79552.1; -
 SQ SEQUENCE 1004 AA; 104286 MW; 7806E7E2D4E3D017 CRC64;

 Query Match 62.1%; Score 36; DB 2; Length 1004;
 Best Local Similarity 70.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 NTLKTPRVGG 10
 Db 224 STLDPRVGG 233
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 RESULT 13
 Q9EMI5 PRELIMINARY; PRT; 1301 AA.
 AC Q9EMI5;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE AMV221.
 GN AMV221.
 OS Anaseta moorei entomopoxvirus (AnEPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
 OC Entomopoxvirus B.
 OX NCBI_TaxID=28321;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20396580; PubMed=10936094;
 RA Bowden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
 RA Moyer R.W.;
 RT "Complete genomic sequence of the Anaseta moorei Entomopoxvirus:
 RT Analysis and Comparison with Other Poxviruses";
 RL Virology 274:120-139(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Bowden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
 RA Moyer R.W.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF250284; AAG02927.1; -
 DR InterPro; IPR006592; RNA_pol_A.
 DR InterPro; IPR000722; RNA_pol_A.
 DR InterPro; IPR007066; RNA_pol_Rpb1_3.
 DR InterPro; IPR007083; RNA_pol_Rpb1_4.
 DR Pfam; PF00623; RNA_pol_Rpb1_2; 1.
 DR Pfam; PF04983; RNA_pol_Rpb1_3; 1.
 DR Pfam; PF05000; RNA_pol_Rpb1_4; 1.
 DR SMART; SM00653; RPOUA_N; 1.
 SQ SEQUENCE 1301 AA; 150298 MW; 3E7D097185975BB7 CRC64;

 Query Match 62.1%; Score 36; DB 12; Length 1301;
 Best Local Similarity 50.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 NTLKTPRVGG 10
 Db 30 NSVKSPLGG 39
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 RESULT 14
 Q8NBV9 PRELIMINARY; PRT; 132 AA.
 ID Q8NBV9
 AC Q8NBV9;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Hypothetical protein FLJ38783.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
 RA Fukushima Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
 RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
 RA Masuho Y., Nagai K., Isogai T.;
 RT "NEDO human cDNA sequencing project";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK096102; BAC04702.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 132 AA; 14581 MW; 22DA60CC890A8211 CRC64;

 Query Match 60.3%; Score 35; DB 4; Length 132;
 Best Local Similarity 60.0%; Pred. No. 51;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 NTLKTPRVGG 10
 Db 65 STLASPLRG 74
 :||| |||||

 RESULT 15
 Q8BC65 PRELIMINARY; PRT; 143 AA.
 ID Q8BC65
 AC Q8BC65;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Major capsid protein (fragment).
 GN Li.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FA93;
 RA Antonsson A., Holmgren V., Hansson B.G.;
 RT "Prevalence and type spectrum of human papillomavirus in normal skin
 RT from three continents";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF542099; AAN28674.1; -
 FT NON_TER 1
 FT NON_TER 143
 SQ SEQUENCE 143 AA; 16103 MW; 7B2EF7C742948DBD CRC64;

 Query Match 60.3%; Score 35; DB 12; Length 143;
 Best Local Similarity 60.0%; Pred. No. 56;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 NTLKTPRVGG 10
 Db 8 NTLEVPKVS 17
 :||| |||||

Search completed: August 28, 2003, 18:37:59
 Job time : 30.9091 secs